



PCT

RAW SEQUENCE LISTING

DATE: 03/25/2003

PATENT APPLICATION: US/09/762,224B

TIME: 13:11:17

Input Set : A:\seq.list.290.00490101.txt

Output Set: N:\CRF4\03252003\I762224B.raw

3 <110> APPLICANT: PURDUE RESEARCH FOUNDATION
 4 Sanders, David
 5 Kuhn, Richard
 6 Jeffers, Scott
 7 Sharkey, Curtis
 8 North, Cynthia
 9 Fischbach, Michael
 11 <120> TITLE OF INVENTION: PSEUDOTYPED RETROVIRUSES AND STABLE CELL LINES FOR THEIR
 PRODUCTION
 13 <130> FILE REFERENCE: 290.00490101
 15 <140> CURRENT APPLICATION NUMBER: 09/762,224B
 16 <141> CURRENT FILING DATE: 2001-02-02
 18 <150> PRIOR APPLICATION NUMBER: US 60/095,242
 19 <151> PRIOR FILING DATE: 1998-08-04
 21 <150> PRIOR APPLICATION NUMBER: US 60/112,405
 22 <151> PRIOR FILING DATE: 1998-12-15
 24 <150> PRIOR APPLICATION NUMBER: PCT/US99/17702
 25 <151> PRIOR FILING DATE: 1999-08-04
 27 <160> NUMBER OF SEQ ID NOS: 8
 29 <170> SOFTWARE: PatentIn version 3.0
 31 <210> SEQ ID NO: 1
 32 <211> LENGTH: 2958
 33 <212> TYPE: DNA
 34 <213> ORGANISM: Ross River virus
 36 <400> SEQUENCE: 1
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138 <210> SEQ ID NO: 2
139 <211> LENGTH: 985
140 <212> TYPE: PRT
141 <213> ORGANISM: Ross River virus
143 <400> SEQUENCE: 2
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148 Cys Ser Ser Pro Cys Tyr Pro Cys Cys Tyr Glu Lys Gln Pro Glu
149 20 25 30
151 Gln Thr Leu Arg Met Leu Glu Asp Asn Val Asn Arg Pro Gly Tyr Tyr
152 35 40 45
154 Glu Leu Leu Glu Ala Ser Met Thr Cys Arg Asn Arg Ser Arg His Arg
155 50 55 60
157 Arg Ser Val Thr Glu His Phe Asn Val Tyr Lys Ala Thr Arg Pro Tyr
158 65 70 75 80
160 Leu Ala Tyr Cys Ala Asp Cys Gly Asp Gly Tyr Phe Cys Tyr Ser Pro
161 85 90 95
163 Val Ala Ile Glu Lys Ile Arg Asp Glu Ala Ser Asp Gly Met Leu Lys

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164          100          105          110
166 Ile Gln Val Ser Ala Gln Ile Gly Leu Asp Lys Ala Gly Thr His Ala
167          115          120          125
169 His Thr Lys Ile Arg Tyr Met Ala Gly His Asp Val Gln Glu Ser Lys
170          130          135          140
172 Arg Asp Ser Leu Arg Val Tyr Thr Ser Ala Ala Cys Ser Ile His Gly
173 145          150          155          160
175 Thr Met Gly His Phe Ile Val Ala His Cys Pro Pro Gly Asp Tyr Leu
176          165          170          175
178 Lys Val Ser Phe Glu Asp Ala Asp Ser His Val Lys Ala Cys Lys Val
179          180          185          190
181 Gln Tyr Lys His Asp Pro Leu Pro Val Gly Arg Glu Lys Phe Val Val
182          195          200          205
184 Arg Pro His Phe Gly Val Glu Leu Pro Cys Thr Ser Tyr Gln Leu Thr
185          210          215          220
187 Thr Ala Pro Thr Asp Glu Glu Ile Asp Met His Thr Pro Pro Asp Ile
188 225          230          235          240
190 Pro Asp Arg Thr Leu Leu Ser Gln Thr Ala Gly Asn Val Lys Ile Thr
191          245          250          255
193 Ala Gly Gly Arg Thr Ile Arg Tyr Asn Cys Thr Cys Gly Arg Asp Asn
194          260          265          270
196 Val Gly Thr Thr Ser Thr Asp Lys Thr Ile Asn Thr Cys Lys Ile Asp
197          275          280          285
199 Gln Cys His Ala Ala Val Thr Ser His Asp Lys Trp Gln Phe Thr Ser
200          290          295          300
202 Pro Phe Val Pro Arg Ala Asp Gln Thr Ala Arg Arg Gly Lys Val His
203 305          310          315          320
205 Val Pro Phe Pro Leu Thr Asn Val Thr Cys Arg Val Pro Leu Ala Arg
206          325          330          335
208 Ala Pro Asp Val Thr Tyr Gly Lys Lys Glu Val Thr Leu Arg Leu His
209          340          345          350
211 Pro Asp His Pro Thr Leu Phe Ser Tyr Arg Ser Leu Gly Ala Glu Pro
212          355          360          365
214 His Pro Tyr Glu Glu Trp Val Asp Lys Phe Ser Glu Arg Ile Ile Pro
215          370          375          380
217 Val Thr Glu Glu Gly Ile Glu Tyr Gln Trp Gly Asn Asn Pro Pro Val
218 385          390          395          400
220 Arg Leu Trp Ala Gln Leu Thr Thr Glu Gly Lys Pro His Gly Trp Pro
221          405          410          415
223 His Glu Ile Ile Gln Tyr Tyr Tyr Gly Leu Tyr Pro Ala Ala Thr Ile
224          420          425          430
226 Ala Ala Val Ser Gly Ala Ser Leu Met Ala Leu Leu Thr Leu Ala Ala
227          435          440          445
229 Thr Cys Cys Met Leu Ala Thr Ala Arg Arg Lys Cys Leu Thr Pro Tyr
230          450          455          460
232 Ala Leu Thr Pro Gly Ala Val Val Pro Leu Thr Leu Gly Leu Leu Cys
233 465          470          475          480
235 Cys Ala Pro Arg Ala Asn Ala Ala Ser Phe Ala Glu Thr Met Ala Tyr
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238 Leu Trp Asp Glu Asn Lys Thr Leu Phe Trp Met Glu Phe Ala Ala Pro
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241 Ala Ala Ala Leu Ala Leu Leu Ala Cys Cys Ile Lys Ser Leu Ile Cys
242          515          520          525
244 Cys Cys Lys Pro Phe Ser Phe Leu Val Leu Leu Ser Leu Gly Ala Ser
245          530          535          540
247 Ala Lys Ala Tyr Glu His Thr Ala Thr Ile Pro Asn Val Val Gly Phe
248 545          550          555          560
250 Pro Tyr Lys Ala His Ile Glu Arg Asn Gly Phe Ser Pro Met Thr Leu
251          565          570          575
253 Gln Leu Glu Val Val Glu Thr Ser Leu Glu Pro Thr Leu Asn Leu Glu
254          580          585          590
256 Tyr Ile Thr Cys Glu Tyr Lys Thr Val Val Pro Ser Pro Phe Ile Lys
257          595          600          605
259 Cys Cys Gly Thr Ser Glu Cys Ser Ser Lys Glu Gln Pro Asp Tyr Gln
260          610          615          620
262 Cys Lys Val Tyr Thr Gly Val Tyr Pro Phe Met Trp Gly Gly Ala Tyr
263 625          630          635          640
265 Cys Phe Cys Asp Ser Glu Asn Thr Gln Leu Ser Glu Ala Tyr Val Asp
266          645          650          655
268 Arg Ser Asp Val Cys Lys His Asp His Ala Ser Ala Tyr Lys Ala His
269          660          665          670
271 Thr Ala Ser Leu Lys Ala Thr Ile Arg Ile Ser Tyr Gly Thr Ile Asn
272          675          680          685
274 Gln Thr Thr Glu Ala Phe Val Asn Gly Glu His Ala Val Asn Val Gly
275          690          695          700
277 Gly Ser Lys Phe Ile Phe Gly Pro Ile Ser Thr Ala Trp Ser Pro Phe
278 705          710          715          720
280 Asp Asn Lys Ile Val Val Tyr Lys Asp Asp Val Tyr Asn Gln Asp Phe
281          725          730          735
283 Pro Pro Tyr Gly Ser Gly Gln Pro Gly Arg Phe Gly Asp Ile Gln Ser
284          740          745          750
286 Arg Thr Val Glu Ser Lys Asp Leu Tyr Ala Asn Thr Ala Leu Lys Leu
287          755          760          765
289 Ser Arg Pro Ser Pro Gly Val Val His Val Pro Tyr Thr Gln Thr Pro
290          770          775          780
292 Ser Gly Phe Lys Tyr Trp Leu Lys Glu Lys Gly Ser Ser Leu Asn Thr
293 785          790          795          800
295 Lys Ala Pro Phe Gly Cys Lys Ile Lys Thr Asn Pro Val Arg Ala Met
296          805          810          815
298 Asp Cys Ala Val Gly Ser Ile Pro Val Ser Met Asp Ile Pro Asp Ser
299          820          825          830
301 Ala Phe Thr Arg Val Val Asp Ala Pro Ala Val Thr Asp Leu Ser Cys
302          835          840          845
304 Gln Val Val Val Cys Thr His Ser Ser Asp Phe Gly Gly Val Ala Thr
305          850          855          860
307 Leu Ser Tyr Lys Thr Asp Lys Pro Gly Lys Cys Ala Val His Ser His
308 865          870          875          880
310 Ser Asn Val Ala Thr Leu Gln Glu Ala Thr Val Asp Val Lys Glu Asp

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311          885          890          895
313 Gly Lys Val Thr Val His Phe Ser Thr Ala Ser Ala Ser Pro Ala Phe
314          900          905          910
316 Lys Val Ser Val Cys Asp Ala Lys Thr Thr Cys Thr Ala Ala Cys Glu
317          915          920          925
319 Pro Pro Lys Asp His Ile Val Pro Tyr Gly Ala Ser His Asn Asn Gln
320          930          935          940
322 Val Phe Pro Asp Met Ser Gly Thr Ala Met Thr Trp Val Gln Arg Leu
323 945          950          955          960
325 Ala Ser Gly Leu Gly Gly Leu Ala Leu Ile Ala Val Val Val Leu Val
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329          980          985
331 <210> SEQ ID NO: 3
332 <211> LENGTH: 2224
333 <212> TYPE: DNA
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336 <400> SEQUENCE: 3
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341 catccacaat agcacattac aggttagtga tgtcgacaaa ctagtttgtc gtgacaaact      180
343 gtcattccaca aatcaattga gatcagttgg actgaatctc gaagggaatg gagtggcaac      240
345 tgacgtgccca tctgcaacta aaagatgggg cttcaggtcc ggtgtcccac caaaggtggt      300
347 caattatgaa gctggtgaat gggctgaaaa ctgctacaat cttgaaatca aaaaacctga      360
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353 tgctttcttc ctgtatgata gacttgcttc cacagttatc taccgaggaa cgactttcgc      540
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357 ccccttgaga gagccggtca atgcaacgga ggaccctgtc agtggctact attctaccac      660
359 aattagatat caggctaccg gttttggaac caatgagaca gagtacttgt tccaggttga      720
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363 tgagacaata tatacaagtg ggaaaaggag caataccacg ggaaaactaa tttggaagg      840
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367 cactagaaaa attcgagtg aagagttgtc ttccacagtt gtatcaaacy gagccaaaaa      960
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393 gttgagacag ctggccaacy agacgactca agctcttcaa ctgttctga gagccacaac      1740
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:7,8

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